

OIPF

#2

RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/900,237

TIME: 10:13:55

Input Set : A:\BB1170 US CIP Seq Listing.txt

Output Set: N:\CRF3\07242001\I900237.raw

P5

ENTERED

2 <110> APPLICANT: Allen, Stephen
 4 <120> TITLE OF INVENTION: Plant Cellulose Synthases
 6 <130> FILE REFERENCE: BB1170 US CIP
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/900,237
 C--> 9 <141> CURRENT FILING DATE: 2001-07-06
 11 <150> PRIOR APPLICATION NUMBER: 60/092,844
 12 <151> PRIOR FILING DATE: 1998-07-14
 14 <150> PRIOR APPLICATION NUMBER: PCT/US99/15871
 15 <151> PRIOR FILING DATE: 1999-07-13
 17 <150> PRIOR APPLICATION NUMBER: 09/720383
 18 <151> PRIOR FILING DATE: 2000-12-21
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: Microsoft Office 97
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1221
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Hordeum vulgare
 29 <400> SEQUENCE: 1
 30 gcacgaggat attcttactg gggtttaaaat gcacgcaaga gggttgatatt caatctactg 60
 31 catgccacca cgaccttggt tcaaggggtc tgcgccaatc aatctctctg accgtctcaa 120
 32 tcaagttctc cgttggtgctc ttgggtcagt tgaaattctg ttagcagac attgtcctat 180
 33 ctggtacaat tacggtgggc gggtgaaact tctggagagg atggcttaca tcaacaccat 240
 34 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttcctg ctatctgtct 300
 35 cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt tctttattct 360
 36 tatgtttgccc tccatctttg ccacgggtat attggagctg cgatggagtgt gtgtcgccat 420
 37 cgaggactgg tggagaaacg agcagttctg gggttattggt ggcacatctg cccatctttt 480
 38 cgcagtggtc caggggtctg tgaaggtggt ggccgggatt gacaccaact tcacggttac 540
 39 ctggaaggca aacgacgagg atggcgattt tgcgtagtta tacgtgttca agtggaccag 600
 40 tctctctcatt cctccgacca ccgtccttgt gattaacctg gtgggcatgg tggcaggcat 660
 41 atcatatgcc atcaacagcg gttaccagtc ttgggggtcca ctcttcggaa agctcttctt 720
 42 ctcaatctgg gtgacccctc atctctaccc ctctctcaag ggtctcatgg ggaagcagaa 780
 43 ccgcacgcca accatcgtea ttgtttggtc catctctcta gectccatct tctccctct 840
 44 gtgggtgaag atcgaccctt tcatatccga taccagaaa gccgtcgcca tggggcagtg 900
 45 tggcgtcaac tgcgtatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg 960
 46 gggttgatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc 1020
 47 cccttcgtgc tgagaagcac aaacogtgaa gcctacgaaa cctgcagcgt acattgtgat 1080
 48 tttttctctc tttcttttct atctgtgata cctgtgtgtt cttcttagag tatattatgt 1140
 49 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt 1200
 50 tgcacaaact cttctgcaaa a 1221
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 53 <211> LENGTH: 304
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Hordeum vulgare
 57 <400> SEQUENCE: 2
 58 His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
 59 1 5 10 15
 61 Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro

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62          20          25          30
64 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
65          35          40          45
67 Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
68          50          55          60
70 Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
71 65          70          75          80
73 Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
74          85          90          95
76 Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
77          100          105          110
79 Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
80          115          120          125
82 Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
83          130          135          140
85 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
86 145          150          155          160
88 Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
89          165          170          175
91 Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
92          180          185          190
94 Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
95          195          200          205
97 Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
98          210          215          220
100 Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
101 225          230          235          240
103 Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
104          245          250          255
106 Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
107          260          265          270
109 Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
110          275          280          285
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116 <211> LENGTH: 3776
117 <212> TYPE: DNA
118 <213> ORGANISM: Zea mays
120 <400> SEQUENCE: 3
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122 aagcgtgtcc ctccccctcc ctactcccg ttctattcca ttcccccca gacgcgcgta 120
123 ccgccgcgcg gcacgcacg cttgccccg gatctggaga tctggtagc ccaggggat 180
124 ggaggccagc gccgggctg tcgccgctc gcacaaccg aacgagctc tgcgtcatccg 240
125 ccgcgatggc gagccaggc cgaagcccat ggaccagcg aacggccag tgtgccagat 300
126 ttgcggcgac gacgtggggc gcaaccccg cgaggagcg ttcgtggcct gcaacgagt 360
127 cgccttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaact 420
128 cccccagtgc aagaccgcct tcaagcgct caaggggtgc gcgcgcgtgc ccggggacga 480
129 ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc 540

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130 ccagtagctc gccagtgcca tgctccacgc ccacatgagc tacggccgcg ggcgcgacct 600
131 cgacggcggtg ccgcagccat tccaccccat ccccaatgtt cccctcctca ccaacggaca 660
132 gatggtcgat gacatccgcg cggaccagca cgccctgtgt cctcgttcg tggggtggcg 720
133 ggggaagagg attcaccctc tcccgtagc ggatcccaac ctctctgtgc aaccgaggtc 780
134 tatggaccct tccaaggatc tcgccgcata tggctacggg agcgtagcat ggaaggagag 840
135 gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaacg atggcggcg 900
136 cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag 960
137 aaagatcccg ctctcttcaa gccaatcaa cccctatagg atgattataa taattcggt 1020
138 agtgggtttg tgtttcttct tccactaccg agttagtcat ccggtgcctg atgcatttgc 1080
139 tttatggctc atattctgtg tctgtgaaat ttggtttgcc atgtcttga ttcttgacca 1140
140 gtttccaaag tggtttccta tcgagaggga aacctatctt gaccggtcga gtttaagggt 1200
141 tgacaaggaa gggcatcctt ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
142 tcccttgaa gaaactccat tggtagctgc taatactgtt ctatctatcc ttctgggtga 1320
143 ttatccagtt gataagttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
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146 caaggtggcg ccaaactttg ttagagaacg gagagcaatg aagagagagt atgaggaatt 1560
147 caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
148 aatgcaggat ggaactccat ggcccgaaa taatgtccgt gatcatcctg gaatgattca 1680
149 ggttttctt ggtcaaagtg gtggccatga tgtggaagga aatgagctgc ctcgattggt 1740
150 ttatgtttca agagaaaaac gggcaggcta caaccatcac aagaaggctg gtgctatgaa 1800
151 tgcattggtc cgagtctctg ctgtactaac taatgctcct tatttgctga acttggtattg 1860
152 tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
153 tttgcttgga aagaaagttt gctatgtgca gtttctcaa agatttgatg ggattgatcg 1980
154 ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aagggttgga 2040
155 tggtagccag ggcccaattt atgtgggtac tggatgtgtc ttcagaaggc aggcattata 2100
156 tggctacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
157 gtgggtgcat tgctgttctg gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220
158 taaacctaaa tttgagaaga taaagaact ttttaagaaa aaggaaaatc aagccctgc 2280
159 atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340
160 tgtaaatcaa cagaagtggg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
161 acttcttgag aatggtggaa cctgaagag tgccagtcca gcttctcttc tgaagggaagc 2460
162 tatacatgtc atcagttgtg gatatgaaga caaacagggc tggggaaaag atattggttg 2520
163 gatttatgga tcagtcacag aagatattct tactgggttt aagatgcaact gccatgggtg 2580
164 gcggtaaat tactgcatac ctaaaagggc cgcttcaaa ggttccgcac ctctcaatct 2640
165 ttccgatcgt ctccaccag ttcttcgggt ggctcttggt tcaattgaaa ttttcttcag 2700
166 caaccactgc cctctctggt atgggtatgg tggtagacta aagttcctgg aaaggttttc 2760
167 gtacattaac tccatcgtat acccttgac atctatcccg ctcttgccct attgcacatt 2820
168 gcctgccatc tgcttgctga cagggaatt tatcacgcca gagcttaaca atgttgccag 2880
169 cctctggttc atgtcacttt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940
170 agtggtgta gcatcgatg actggtggag aaacgagcag ttttggtca ttggaggcgt 3000
171 gtcttcacat ctctttgctg tgttccaggg actcctcaag gtcatactg gtgtagacac 3060
172 gagcttcaat gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120
173 caaatggagc acccttctga tacctccgac aaccctgctc ctactgaact tcattggagt 3180
174 ggtagctggc atctccaatg cgatcaacaa cgatgatgaa tcatggggcc cctgttctcg 3240
175 gaagctcttc tttgcatttt gggtagctgt ccatctttac ccgttctca aggtctggt 3300
176 tgggagggag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
177 cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtccctgtt 3420
178 ggaggagtgt ggtctgatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480

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179 tgggtcgaaga agtattttttg cagatgtttt gtgcccataat ttcttttttc aattttttgtc 3540
180 cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgatattt cttttgttcc 3600
181 atgggtggtgg tgggtggtggg cggctcagcc tcgtgagtgac agtattgggc aaaccggagg 3660
182 ctgcccgaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
183 caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 1148
187 <212> TYPE: PRT
188 <213> ORGANISM: Zea mays
190 <400> SEQUENCE: 4
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192 1 5 10 15
194 Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
195 20 25 30
197 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
198 35 40 45
200 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
201 50 55 60
203 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
204 65 70 75 80
206 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
207 85 90 95
209 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
210 100 105 110
212 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
213 115 120 125
215 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
216 130 135 140
218 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
219 145 150 155 160
221 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
222 165 170 175
224 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
225 180 185 190
227 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
228 195 200 205
230 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
231 210 215 220
233 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
234 225 230 235 240
236 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
237 245 250 255
239 Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
240 260 265 270
242 Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
243 275 280 285
245 Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
246 290 295 300
248 Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg

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249 305          310          315          320
251 Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
252          325          330          335
254 Ile Ile Arg Leu Val Val Leu Cys Phe Phe His Tyr Arg Val Met
255          340          345          350
257 His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
258          355          360          365
260 Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
261          370          375          380
263 Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
264 385          390          395          400
266 Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
267          405          410          415
269 Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
270          420          425          430
272 Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
273          435          440          445
275 Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
276          450          455          460
278 Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
279 465          470          475          480
281 Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
282          485          490          495
284 Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
285          500          505          510
287 Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
288          515          520          525
290 Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
291          530          535          540
293 Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
294 545          550          555          560
296 Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
297          565          570          575
299 Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
300          580          585          590
302 His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
303          595          600          605
305 Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
306          610          615          620
308 Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
309 625          630          635          640
311 Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
312          645          650          655
314 Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe
315          660          665          670
317 Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val
318          675          680          685
320 Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala
321          690          695          700

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,237

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Input Set : A:\BB1170 US CIP Seq Listing.txt

Output Set: N:\CRF3\07242001\I900237.raw

L:8 M:270 C: Current Application Number differs, Replaced Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1289 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:1289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1893 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20